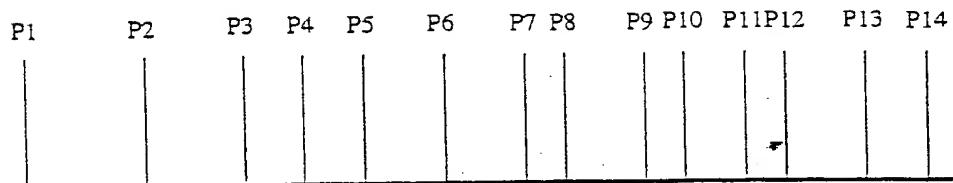
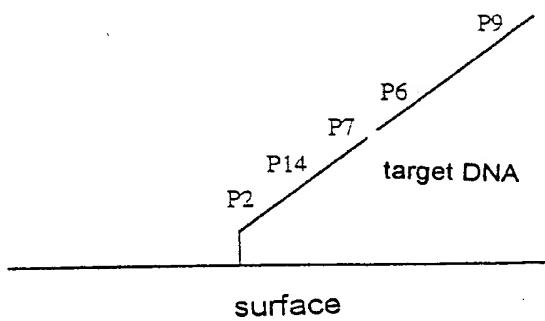


1. Mass distribution of the probes



2. Hybridization



3. Mass distribution of the hybridized probes

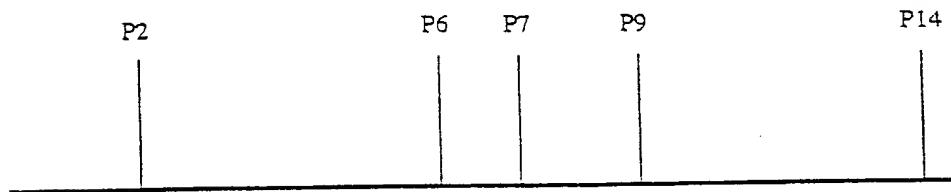
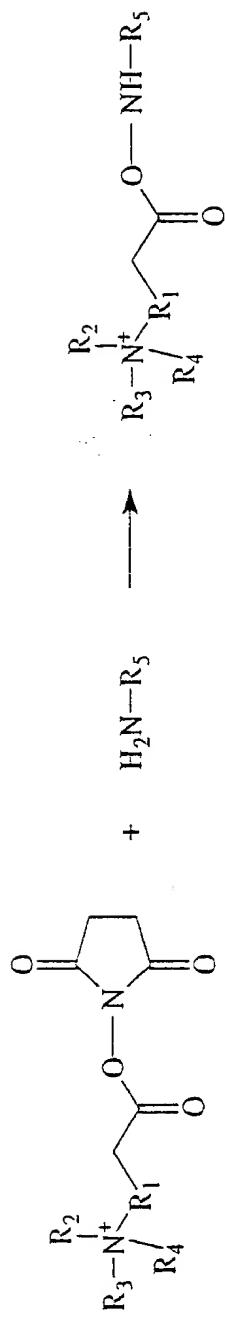
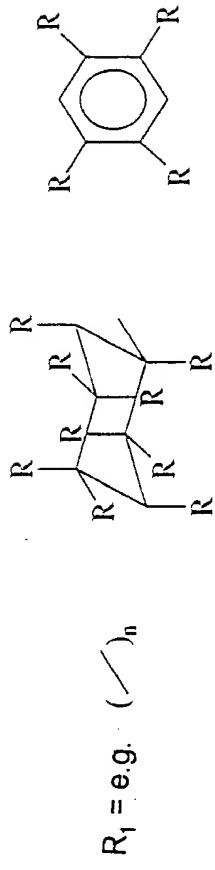


Fig. 1

N-terminal mass/charge tagging



$R =$ e.g. alkyl, -CH₃, -C₂H₅, -C₃H₇, -C₄H₉ etc.

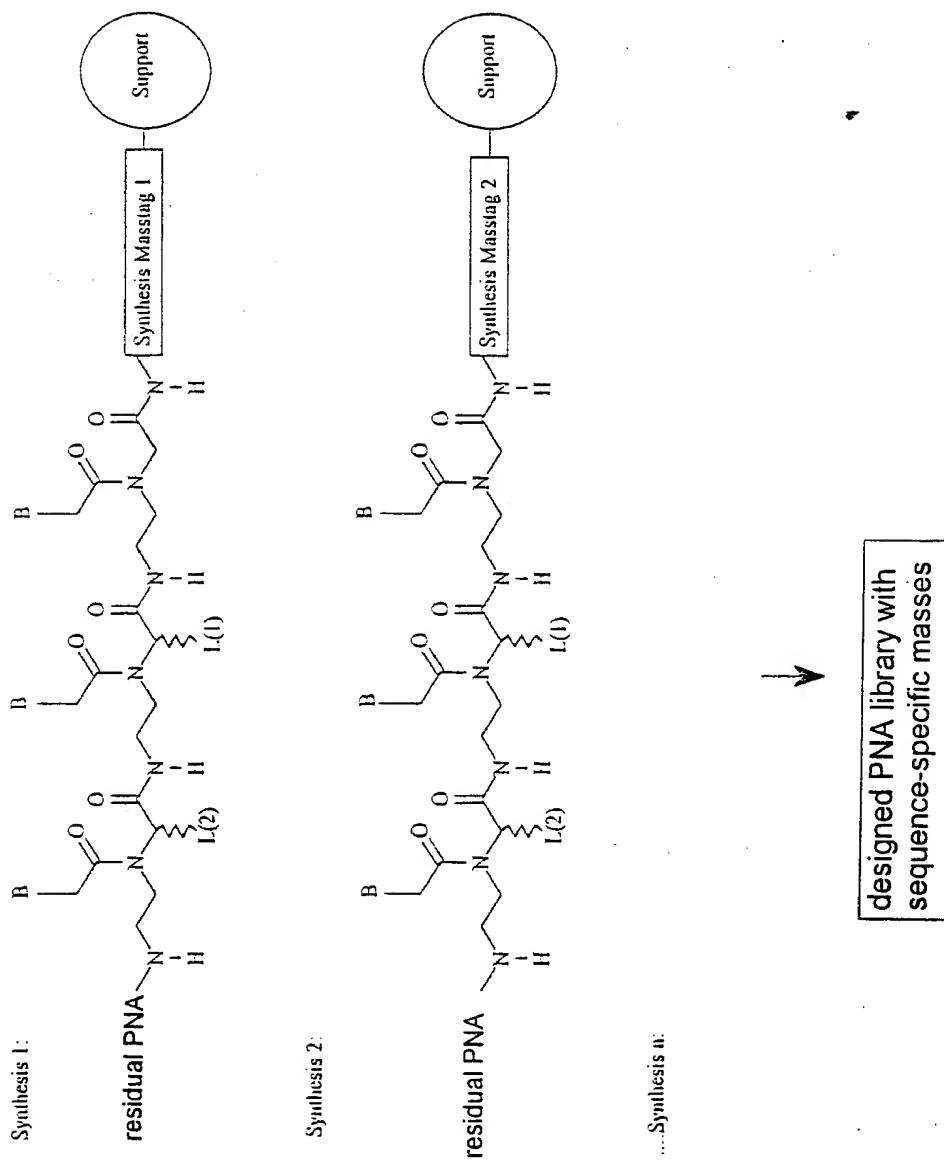


$\text{R}_{24} =$ e.g. alkyl, substituted alkyl

$\text{R}_5 =$ e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acid

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$B = \text{adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues}$

$L(n)$ are various sets of substituents, selected specifically for each base, which are inserted in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS.

Fig. 3

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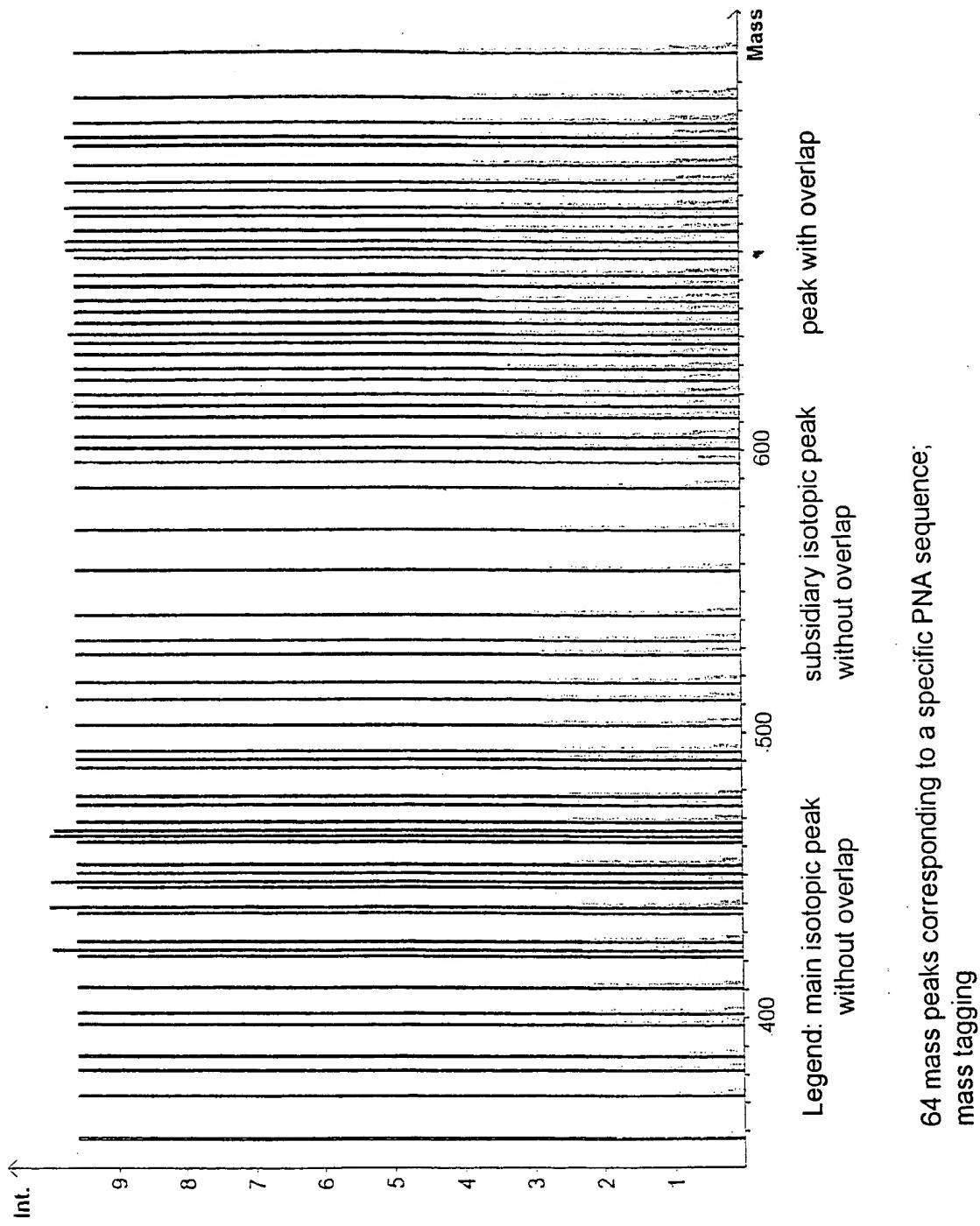


Fig. 4

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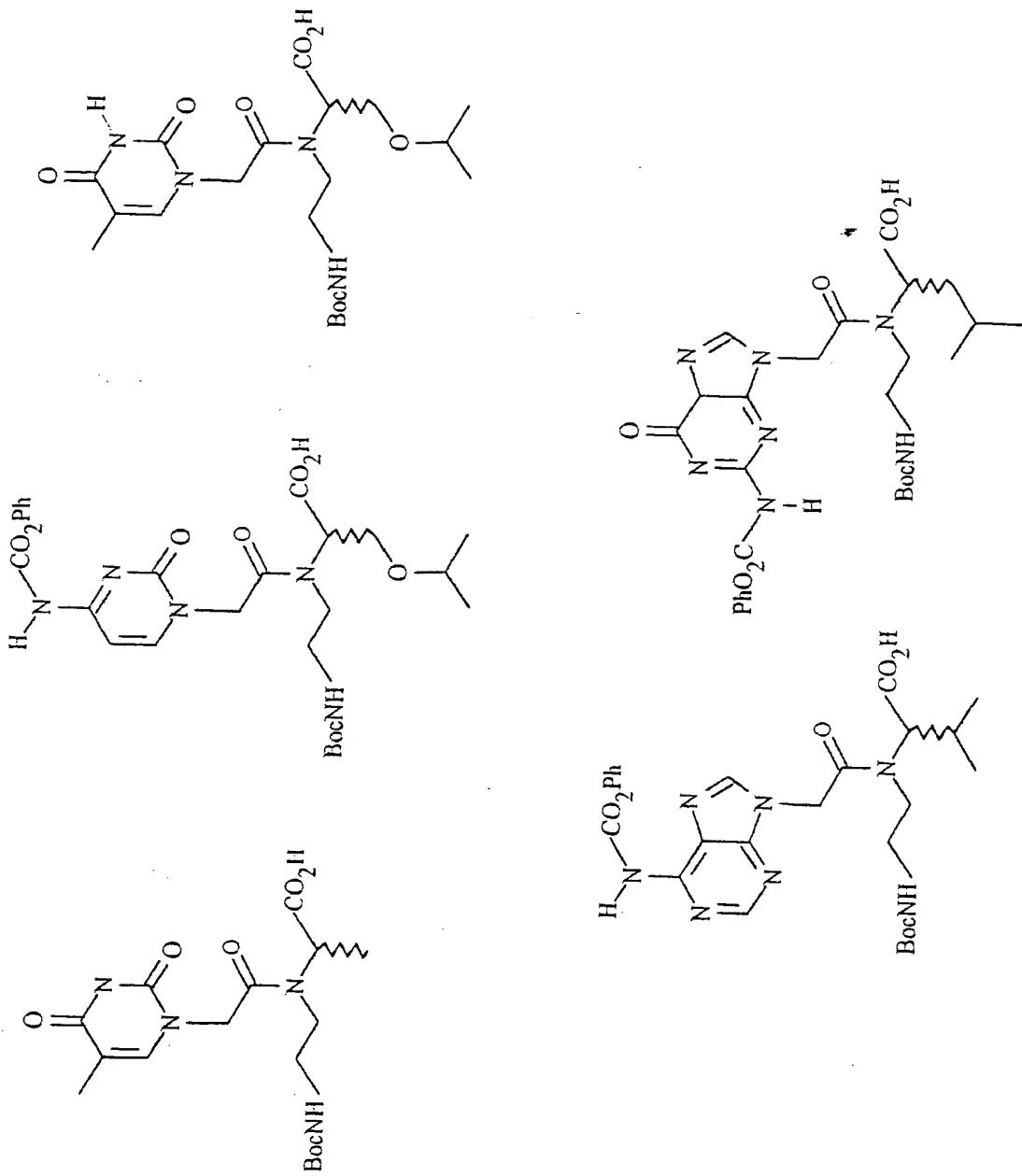


Fig. 5

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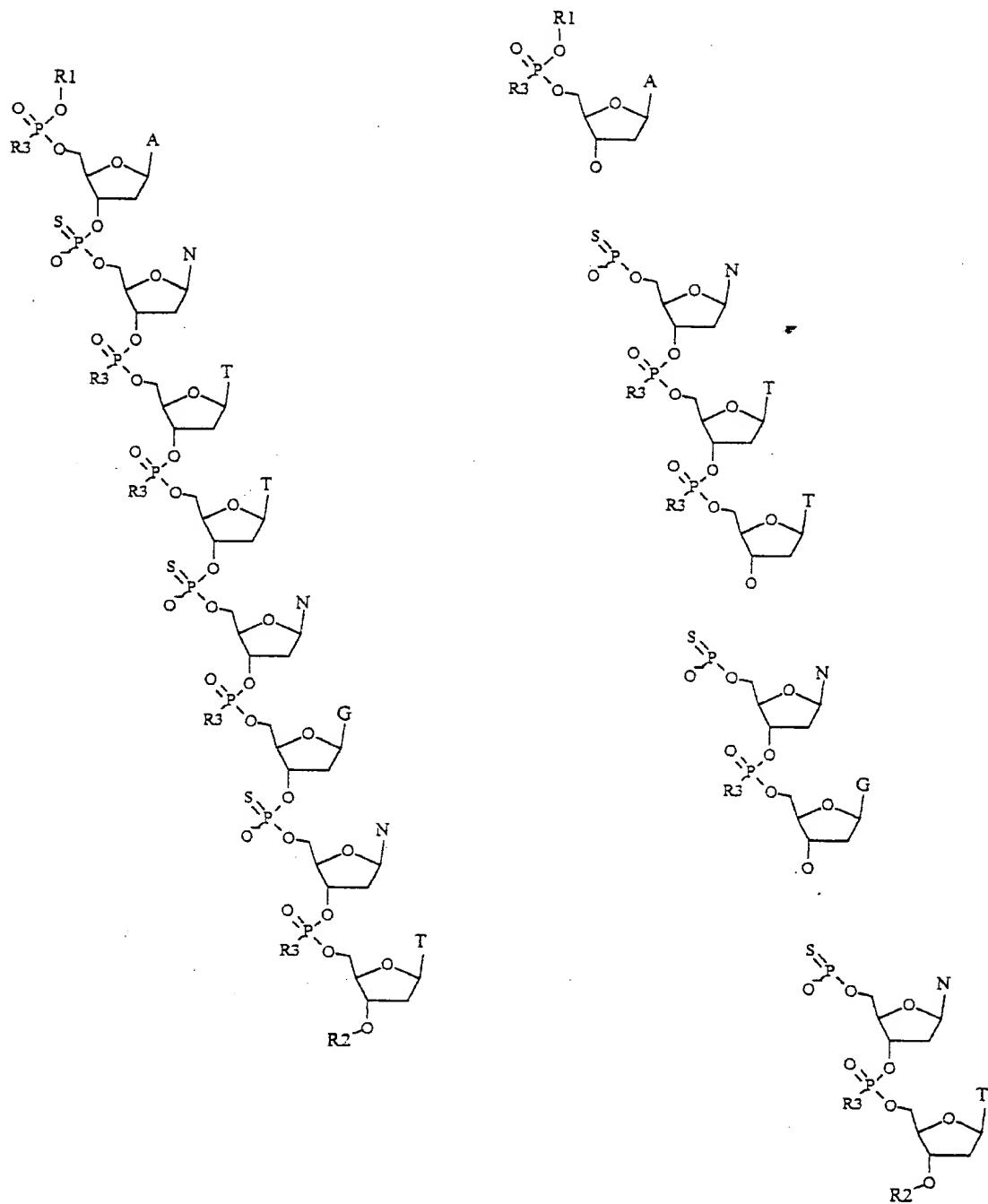


Fig. 6